



SEQUENCE LISTING

<110> Loughney & Kate
<120> Phosphodiesterase 10
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<140> 10/083,620
<141> 2002-02-26
<150> 09/256,000
<151> 1999-02-23
<150> 60/075,508
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<170> PatentIn Ver. 2.0

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<222> (26)..(1423)

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 aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 100
 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 10 15 20 25

 atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
 30 35 40

 aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
 Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
 45 50 55

 gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
 60 65 70

 tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
 75 80 85

 agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
 90 95 100 105

 aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc. 388
 Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
 110 115 120

 tct cca gag acc atc gag gcc ctg cggt aag ccg acc ttt gac gtc tgg 436
 Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp

125	130	135	
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His 140	145	150	484
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg 155	160	165	532
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His 170	175	180	580
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val 190	195	200	628
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile 205	210	215	676
cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn 220	225	230	724
aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn 235	240	245	772
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile 250	255	260	820
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly 270	275	280	868
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp 285	290	295	916
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu 300	305	310	964
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile 315	320	325	1012
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val 330	335	340	1060
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser 350	355	360	1108
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg 365	370	375	1156
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc			1204

Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
380	385	390	
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag	1252		
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
395	400	405	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag	1300		
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
410	415	420	425
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac	1348		
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp			
430	435	440	
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat	1396		
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp			
445	450	455	
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc gggggggcg	1443		
Val Lys Asn Ser Glu Gly Asp Cys Ala			
460	465		
gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtcaggg aagagctgcc	1503		
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<212> PRT

<213> Homo sapiens

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Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala		
35	40	45

Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu		
50	55	60

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys			
65	70	75	80

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys		
85	90	95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp		
100	105	110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala		
115	120	125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met		
130	135	140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp			
145	150	155	160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
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Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
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Cys Ala
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gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccg 180
gatcgntacg aggagctgaa gcggntagat gacgccatga aagag 225

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gnaaccacca ctgcggcggt gccttccaga tcctcgccga gcctgagtgn aacatcttct 120
ccaacatccc acctgatggg ttcaaggcaga tccgacag 158

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ttccccgtggc cccgttcattt gaccgagaca aagtgcacaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt taaaacagtg accaagctct tccccatggg 240

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cttgaagcg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
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ccagaactgc agccacgccc cccgtttcc tcaggcacag tctccttcac tgttttcac 180
atctctgnntt ctctctctgg ganttnctgg tgggccccag aacgtcaagc tgtcagtnntt 240
cttctgttaac tnttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgtatntt 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagtt 360
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<212> DNA
<213> Mus musculus

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ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagttt 240
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<210> 10
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<212> DNA
<213> Mus musculus

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ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaa tgaccaaag aacagccaa ttgggttcat caagtttgc 240
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cctgggtgg cagccaggcg gttggctgg cgaanaggtt catccatcca gtcacactg 180
gaagccaaga agctgaaatt attagtcttc ttgaaacaag gtgtctataa atctggttt 240
caaggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggcctcct 300
tcatggtcag aggacgcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360
aagtgggtg aaggccgtgc attctcgctc tgntttcca gagaattaaa accagtttc 420
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<220>
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<222> (99)..(443)

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Cys His Cys Leu Leu His
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
10 15 20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
25 30 35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 260
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
40 45 50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 308
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
55 60 65 70

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cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 356
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
75 80 85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 404
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
90 95 100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
105 110 115

ggggggcggtg gctgcagttc tggacggctt ggccgagctg cgccggatcc ttgtgcaggg 513

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ctgatacaaa aaaaaaaaaaaa aaaaaaa 599

<210> 13
<211> 115
<212> PRT
<213> Homo sapiens

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Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
85 90 95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
100 105 110

Asp Cys Ala
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<213> Artificial Sequence

<220>
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<210> 15

<211> 28
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 <220>
 <223> Description of Artificial Sequence: primer

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(1066)

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 Ala Leu Glu
 1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
 His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
 5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
 Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
 55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
 Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
 70 75 80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg 403
 Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
 85 90 95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg 451
 Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
 100 105 110 115

gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc 499
 Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
 120 125 130

cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc 547
 Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile
 135 140 145

ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa	595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys	
150 155 160	
gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg	643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu	
165 170 175	
ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt	691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg	
180 185 190 195	
cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat	739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr	
200 205 210	
ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg	787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro	
215 220 225	
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc	835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe	
230 235 240	
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc	883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe	
245 250 255	
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat	931
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp	
260 265 270 275	
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag	979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln	
280 285 290	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag	1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu	
295 300 305	
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc	1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala	
310 315 320	
ggggggcggtg gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg	1136
aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca	1196
ctgataaaaa aaaaaaaaaaag gaattcatga tgctgtacag aatttttattt ttaaactgtc	1256
ttttaaataa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaaaaa	1303

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<211> 320
<212> PRT
<213> Homo sapiens

<400> 17
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20

25

30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
 35 40 45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
 50 55 60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65 70 75 80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
 85 90 95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
 100 105 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
 130 135 140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 225 230 235 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
 245 250 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
 260 265 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
 275 280 285

Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
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Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 305 310 315 320

<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> (74)..(1672)

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cgccgggcgc agg atg gga tcc ggc tcc tcc agc tac cgg ccc aag gcc 109
Met Gly Ser Gly Ser Ser Tyr Arg Pro Lys Ala
1 5 10

atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
15 20 25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
30 35 40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg 253
Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
45 50 55 60

gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac 301
Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr
65 70 75

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 349
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
80 85 90

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 397
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
95 100 105

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gtc cta 445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
110 115 120

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
125 130 135 140

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 541
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
145 150 155

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
160 165 170

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
175 180 185

tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg 685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
190 195 200

ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac 733
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
205 210 215 220

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg 781

Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg			
225	230	235	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac		829	
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His			
240	245	250	
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc		877	
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val			
255	260	265	
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc		925	
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile			
270	275	280	
cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac		973	
Leu Met Thr Ala Ala Cys His Asp Leu Asp His Pro Gly Tyr Asn			
285	290	295	300
aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat		1021	
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn			
305	310	315	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc		1069	
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile			
320	325	330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg		1117	
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly			
335	340	345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac		1165	
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp			
350	355	360	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag		1213	
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu			
365	370	375	380
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att		1261	
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile			
385	390	395	
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc		1309	
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val			
400	405	410	
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc		1357	
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser			
415	420	425	
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga		1405	
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
430	435	440	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc		1453	
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
445	450	455	460
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag		1501	
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
465	470	475	

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag	1549		
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
480	485	490	
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac	1597		
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp			
495	500	505	
agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat	1645		
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp			
510	515	520	
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc gggggcgctg	1692		
Val Lys Asn Ser Glu Gly Asp Cys Ala			
525	530		
gctgcagttc tggacggct ggccgagctg cgccggatcc ttgtcaggg aagagctgcc	1752		
ctggcacct ggcaccacaa gaccatgttt tctaagaacc attttgcata ctgataaaaa	1812		
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atatattctt atacg	1887		
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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser			
20	25	30	
Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn			
35	40	45	
Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp			
50	55	60	
Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro			
65	70	75	80
Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val			
85	90	95	
Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu			
100	105	110	
Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val			
115	120	125	
Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp			
130	135	140	
Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn			
145	150	155	160
Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro			
165	170	175	

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205
 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255
 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270
 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285
 Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300
 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
 305 310 315 320
 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
 325 330 335
 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
 340 345 350
 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415
 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
 420 425 430
 Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
 435 440 445
 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
 450 455 460
 Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
 465 470 475 480
 Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
 485 490 495
 Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
 500 505 510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
515 520 525

Glu Gly Asp Cys Ala
530

<210> 20

<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1741)

<400> 20

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Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
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tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cggtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa 529
Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att 577
Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile

180	185	190	
aag aag atg agg gag ctg gcg gcc aga agc agc agg acc aac tgc Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195	200	205	625
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210	215	220	673
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225	230	235	721
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245	250	255	769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260	265	270	817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275	280	285	865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290	295	300	913
tcc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305	310	315	961
cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325	330	335	1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340	345	350	1057
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355	360	365	1105
gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu 370	375	380	1153
tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg 385	390	395	1201
cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala 405	410	415	1249
gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser 420	425	430	1297
aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt			1345

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys			
435	440	445	
gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg	1393		
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val			
450	455	460	
gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca	1441		
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser			
465	470	475	480
gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag	1489		
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys			
485	490	495	
gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt	1537		
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe			
500	505	510	
gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag	1585		
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln			
515	520	525	
cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat	1633		
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp			
530	535	540	
gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg	1681		
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly			
545	550	555	560
gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa	1729		
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu			
565	570	575	
gga gac tgt gcc tgaggaaagc gggggcggtg gctgcagtgc tggacgggct	1781		
Gly Asp Cys Ala			
580			
ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctggcacct ggcaccacaa	1841		
gaccatgttt tctaagaacc attttgttca ctgataaaaaaaa aaaaaaaaaa ggaattcatg	1901		
atgctgtaca gaattttatt tttaaactgt cttttaata atatattctt atacggaaaa	1961		
aaaaaa	1967		
<210> 21			
<211> 580			
<212> PRT			
<213> Homo sapiens			
<400> 21			
Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr			
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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu			
20	25	30	
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val			
35	40	45	

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
 50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
 85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
 100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
 115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
 130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
 145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
 165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
 180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
 195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
 210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
 225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
 245 250 255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
 260 265 270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
 275 280 285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
 290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
 305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
 325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
 340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
 355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
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Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
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Gly Asp Cys Ala
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (164)..(1453)

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 ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc 175
 Met Gly Ser Gly
 1

tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
 Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
 5 10 15 20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271

Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met			
25	30	35	
gac ctg ttc tgc atc gcc acc ggc ctg cct cg aac acg acc atc tcc		319	
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser			
40	45	50	
ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc		367	
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro			
55	60	65	
gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag		415	
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys			
70	75	80	
caa ctc tcc gag aga gaa tta atc cag agc gtg ctg gcg cag gtt		463	
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val			
85	90	95	100
gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa		511	
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu			
105	110	115	
gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga		559	
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly			
120	125	130	
cta aaa gtg gtg gag att gag aaa tgc aag agt gac att aag aag atg		607	
Leu Lys Val Val Glu Ile Glu Lys Cys Ser Asp Ile Lys Lys Met			
135	140	145	
agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag		655	
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys			
150	155	160	
tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt		703	
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val			
165	170	175	180
ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg		751	
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu			
185	190	195	
cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg		799	
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu			
200	205	210	
agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc agg gac ttc		847	
Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe			
215	220	225	
agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac		895	
Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp			
230	235	240	
aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg		943	
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val			
245	250	255	260
gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc cag gag aag		991	
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys			
265	270	275	

ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc atc tgc cac	1039
Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His	
280	285
290	
gat ctg gac cat ccc ggc tac aac aac acg tac cag atc aat gcc cgc	1087
Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg	
295	300
305	
aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac	1135
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His	
310	315
320	
cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag tgc aac atc	1183
His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile	
325	330
335	340
ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg	1231
Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met	
345	350
355	
atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg	1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met	
360	365
370	
gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag	1327
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu	
375	380
385	
cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct	137.5
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser	
390	395
400	
aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta	142.3
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu	
405	410
415	420
tta gag gaa tat ttt atg cag agc gac cgt gaga	1457
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg	
425	430

<210> 23

<211> 430

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp	
1	5
10	15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser	
20	25
30	

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn	
35	40
45	

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp	
50	55
60	

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro	
65	70
75	80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val

85

90

95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
 305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
 325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
 340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg

420

425

430

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG epitope

<400> 24
Asp Thr Lys Asp Asp Asp Asp Lys
1 5

<210> 25
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 25
tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact 54

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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cgaggagtca acttcttg 18